

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 20, 2000, 02:31:50 ; Search time 78.25 Seconds
(without alignments)
2.997 Million cell updates/sec

Title: US-09-185-908-2

Sequence: 1 IYSY 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues
1 number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	47	2	hypothetical prote
2	22	100.0	89	2	cyclin-dependent k
3	22	100.0	91	2	1-aminocyclopropan
4	22	100.0	91	2	1-aminocyclopropan
5	22	100.0	92	2	pit2 protein (clon
6	22	100.0	95	2	hypothetical prote
7	22	100.0	97	2	ig light chain v r
8	22	100.0	98	2	ig light chain v r
9	22	100.0	99	2	NADH dehydrogenase
10	22	100.0	101	2	ig kappa chain v r
11	22	100.0	101	2	hypothetical prote
12	22	100.0	106	2	ig kappa chain v r
13	22	100.0	106	2	hypothetical prote
14	22	100.0	107	2	ig kappa chain v r
15	22	100.0	108	1	ig kappa chain v r
16	22	100.0	108	1	ig kappa chain v r
17	22	100.0	119	2	conserved hypotet
18	22	100.0	119	2	transporling AT
19	22	100.0	121	2	phospholipase A2 (
20	22	100.0	122	2	phospholipase A2 (
21	22	100.0	122	2	phospholipase A2 (
22	22	100.0	122	2	phospholipase A2 (
23	22	100.0	125	2	hypothetical prote
24	22	100.0	128	2	ig kappa chain pre
25	22	100.0	134	2	ig kappa chain pre
26	22	100.0	134	2	hypothetical prote
27	22	100.0	137	2	phospholipase A2 (
28	22	100.0	138	2	phospholipase A2 (
29	22	100.0	138	2	phospholipase A2 (

30	22	100.0	141	2	hypothetical prote
31	22	100.0	145	2	cryptogene protein
32	22	100.0	146	1	phospholipase A2 (
33	22	100.0	146	2	ig heavy chain var
34	22	100.0	146	2	hypothetical prote
35	22	100.0	149	2	hypothetical prote
36	22	100.0	150	1	hypothetical prote
37	22	100.0	150	2	E6 protein - human
38	22	100.0	153	2	thyroxine-binding
39	22	100.0	155	2	hypothetical 17k p
40	22	100.0	155	2	hypothetical prote
41	22	100.0	171	2	hypothetical prote
42	22	100.0	172	2	n-terminal acetyl
43	22	100.0	172	2	probable acetyl
44	22	100.0	182	2	housekeeping prote
45	22	100.0	183	2	hypothetical prote

ALIGNMENTS

```
RESULT 1
D64402
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: D64402
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek,
; Ron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, -1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A:Reference number: A64300, MUID:96337999
A:Accession: D64402
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-47 <BDL>
A:Cross-references: GB:U67526; GB:L77117; NID:g1591508; PIDN:AAB98832.1; PID:g1591509
C:Genetics:
A:Map position: REV742333-742190
A:Start codon: GTG

Query Match 100.0%; Score 22; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. NO. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYSY 4
Db 33 IYSY 36

RESULT 2
I52695
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 10-Jul-1998
C:Accession: I52695
R:Khatib, Z.A.; Matsushima, H.; Valentine, M.; Shapiro, D.N.; Sherr, C.J.; Look, A.T.
Cancer Res. 53, 5535-5541, 1993
A:Title: Complementation of the CDK4 gene with MDM2 and GLI in human sarcomas.
A:Reference number: I52695; MUID:94036854
A:Accession: I52695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-89 <RES>
A:Cross-references: GB:S67448; NID:g456768
C:Genetics:
A:Gene: GDB:CDK4
A:Cross-references: GDB:204022; OMIM:123829
A:Map position: 12q13-12q13
```

;Introns: 24/3; 80/3
;Superfamily: kinase-related transforming protein; protein kinase homology
;Keywords: Phosphotransferase
;1-89/Domains: protein kinase homology (fragment) <KIN>

Query Match 100.0%; Score 22; DB 2; Length 89;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
||||
70 IYSY 73

RESULT 3
S51643

-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - garden pea (fragment)

;Species: Pisum sativum (garden pea)

;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 03-Dec-1999

;Accession: S51643

;Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine

;Status: preliminary

;Submitted to the EMBL Data Library, December 1994

;Description: Sequential induction of ethylene biosynthetic enzymes by indole-3-acetic

;Reference number: S51643

;Accession: S51643

;Molecule type: mRNA

;Residues: 1-91 <PEC>

;Cross-references: EMBL:X83105; NID:9602079; PIDN:CAA58167.1; PID:9602080

;Superfamily: 1-aminocyclopropane-1-carboxylate synthase

;Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine

Query Match 100.0%; Score 22; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
||||
78 IYSY 81

RESULT 4
S5734

-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (clone ACS-2) - garden pea (fragment)

;Species: Pisum sativum (garden pea)

;Date: 28-Oct-1995 #sequence_revision 24-May-1996 #text_change 03-Dec-1999

;Accession: S55734

;Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine

;Status: preliminary

;Submitted to the EMBL Data Library, December 1995

;Description: Sequential induction of the ethylene biosynthetic enzymes by indole-3-acetic acid

;Reference number: S55734; MUID:95322591

;Accession: S55734

;Molecule type: mRNA

;Residues: 1-91 <PEC>

;Superfamily: 1-aminocyclopropane-1-carboxylate synthase

;Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine

Query Match 100.0%; Score 22; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
||||
78 IYSY 81

RESULT 5
S3677

Protein (clone PAL141), PI starvation induced - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C:Accession: T03677

R:Zakari, B.; Yamamoto, Y.; Matsumoto, H.

Physiol. Plantarum 93, 11-18, 1995

A:Title: Cloning and sequencing of the cDNAs induced by aluminium treatment and PI st

A:Reference number: Z14998

A:Accession: T03677

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-92 <EZA>

A:Cross-references: EMBL:D29681; NID:d1019588; PID:d1006713

A:Experimental source: strain Samsun; clone PAL141

C:Genetics:

A:Gene: pit2

Query Match 100.0%; Score 22; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
||||
48 IYSY 51

RESULT 6
S00966

Hypothetical protein 8 - yeast (Kluveromyces marxianus var. lactis) plasmid pgk12

C:Species: Kluveromyces marxianus var. lactis, Candida sphaerica

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 29-Oct-1999

C:Accession: S00966

R:Tommasino, M.; Ricci, S.; Galeotti, C.L.

Nucleic Acids Res. 16, 5863-5878, 1988

A:Title: Genome organization of the killer plasmid pgk12 from Kluveromyces lactis.

A:Reference number: S00959; MUID:88289339

A:Accession: S00966

A:Molecule type: DNA

A:Residues: 1-95 <TOM>

A:Cross-references: EMBL:X07776; NID:92868; PIDN:CAA30610.1; PID:92877

C:Genetics:

A:Genome: plasmid

Query Match 100.0%; Score 22; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
||||
37 IYSY 40

RESULT 7
PH1068

Ig light chain V region (clone s17.166) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1068

R:Tillman, D.M.; Jou, N.T.; Hall, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1068

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-97 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 100.0%; Score 22; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IYSY 4
|||||
Db 28 IYSY 31

RESULT 8

PH1069
Ig light chain V region (clone 185-cl) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1069
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1069
A:Status: nucleic acid sequence not shown
A:Residues: 1-98 <TIL>
A:Molecule type: mRNA
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin

Query Match 100.0%; Score 22; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IYSY 4
|||||
Db 29 IYSY 32

RESULT 9

SS9145
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - land snail mitochondrion
C:Species: mitochondrion Albinaria coerulea (land snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C:Accession: SS9145
R:Hatzioglou, E.; Rodakis, G.C.; Lecanidou, R.
Genetics 140, 1353-1366, 1995
A:Title: Complete sequence and gene organization of the mitochondrial genome of the land
A:Reference number: SS9143; MUID:96120351
A:Accession: SS9145
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <HAT>
A:Cross-references: EMBL:X03390; NID:975668; PIDN:CA58298.1; PID:975671
C:Genetics:
A:Gene: ND4L
A:Genome: mitochondrion
A:Genetic code: SGC4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 100.0%; Score 22; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4
|||||
Db 3 IYSY 6

RESULT 10

SS20810
Ig kappa chain V region (hybridoma C8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20810
R:Hoogenboom, R.; Dubois, P.; Raus, J.; Voelckaert, G.
Submitted to the EMBL Data Library, September 1990
A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine an
A:Reference number: S20809
A:Accession: S20810
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-101 <HOO>

A:Cross-references: EMBL:X54693; NID:950251; PIDN:CA538509.1; PID:950252
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 100.0%; Score 22; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4
|||||
Db 22 IYSY 25

RESULT 11

G72308
hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: G72308
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: G72308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <ARN>
A:Cross-references: GB:AE001761; GB:AE000512; NID:94981529; PID:94981533; TIGR:TM0993
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0993

Query Match 100.0%; Score 22; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4
|||||
Db 77 IYSY 80

RESULT 12

B47329
Ig kappa chain V region (PRI) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 16-Aug-1996
C:Accession: B47329
R:Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993
A:Title: A recombinant immunotoxin that is active on prostate cancer cells and that i
A:Reference number: A47329; MUID:93133825
A:Accession: B47329
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-106 <BRI>
A:Experimental source: Balb/c
A>Note: sequence modified after extraction from NCBI backbone
A:Note: sequence extracted from NCBI backbone (NCBIN:122874)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

```
Query Match
Best Local Similarity 100.0%; Score 22; DB 2; Length 106;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32

RESULT 13
Hypothetical protein APE0530 - Aeropyrum pernix (strain K1)
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
Accession: E72750
Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kawai, Res. 6, 83-101, 1999
Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
Reference number: A72450; MID:99310339
Accession: E72750
Status: preliminary
Molecule type: DNA
Residues: 1-106 <KAW>
Cross-references: DDBJ:AP000059; NID:95103911; PIDN:BA97497.1; PID:d1043283; PID:95103911
Experimental source: strain K1
Gene: APE0530

Query Match
Best Local Similarity 100.0%; Score 22; DB 2; Length 106;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
63 IYSY 66

RESULT 14
Ig kappa chain V region (J34/32) - mouse
Accession: S24290
Species: Mus musculus (house mouse)
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Accession: S24290
Inchamont, B.
Submitted to the EMBL Data Library, September 1991
Description: Cloning and sequencing of the cDNA coding for the variable regions of the kappa chain V region.
Reference number: S24287
Accession: S24290
Status: preliminary
Molecule type: mRNA
Residues: 1-107 <MON>
Cross-references: EMBL:X62704; NID:951693; PIDN:CAA44580.1; PID:e42102; PID:g1333967
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 22; DB 2; Length 107;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32

RESULT 15
Ig kappa chain V region (M149) - mouse
Accession: S24290
Species: Mus musculus (house mouse)
```

```
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Aug-1996
C:Accession: A01919
R:Appella, E.; Alvarez, V.L.
Mol Immunol 17, 1507-1513, 1980
A:Title: Amino acid sequence of the variable region of M149 mouse myeloma light chain
A:Reference number: A01919; MID:82057806
A:Accession: A01919
A:Molecule type: protein
A:Residues: 1-108 <APP>
A:Experimental source: strain BALB/c
A>Note: this chain was isolated from a myeloma protein
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chains and two heavy (H) chains. In some cases, such as IgA and IgM, the subunits associate into dimers.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 100.0%; Score 22; DB 1; Length 108;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32
```

Search completed: June 20, 2000, 02:31:52
Job time: 8785 sec